

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/885,189

OIPE

DATE: 05/02/2002  
TIME: 15:07:48

INPUT SET: S36845.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Chris SOMERVILLE  
Pierre BROUN  
Frank VAN DE LOO

(ii) TITLE OF INVENTION: Production of Hydroxylated Fatty Acids in  
Genetically Modified Plants

(iii) NUMBER OF SEQUENCES: 15

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: PILLSBURY MADISON & SUTRO, LLP  
(B) STREET: 1100 NEW YORK AVENUE, N.W.  
(C) CITY: WASHINGTON  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 20005-3918

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: MS-DOS/PC-DOS  
(D) SOFTWARE: Word Perfect 5.1

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/885,189  
(B) FILING DATE: 21-June-2001  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/597,313D  
(B) FILING DATE: February 6, 1996

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/530,862  
(B) FILING DATE: September 20, 1995

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/320,982  
(B) FILING DATE: October 11, 1994

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/314,596  
(B) FILING DATE: September 26, 1994

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49 (2) INFORMATION FOR SEQ ID NO:1:

50

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 543 nucleotides

53 (B) TYPE: nucleotide

54 (C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

56

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

58

59 TATTGGCACC GGCGGCACCA TTCCAACAAT GGATCCCTAG AAAAAGATGA AGTCTTTGTC 60

60

61 CCACCTAAGA AAGCTGCAGT CANATGGTAT GTCAAATACC TCAACAACCC TCTTGACGC 120

62

63 ATTCTGGTGT TAACAGTTCA GTTTATCCTC GGGTGGCCTT TGTATCTAGC CTTTAATGTA 180

64

65 TCAGGTAGAC CTTATGATGG TTTCGCTTCA CATTTCTTCC CTCATGCACC TATCTTTAAG 240

66

67 GACCGTGAAC GTCTCCAGAT ATACATCTCA GATGCTGGTA TTCTAGCTGT CTGTTATGGT 300

68

69 CTTTACCGTT ACGCTGCTTC ACAAGGATTG ACTGCTATGA TCTGCGTCTA CGGAGTACCG 360

70

71 CTTTTGATAG TGAACTTTTT CCTTGTCTTG GTCACCTTCT TGCAGCACAC TCATCCTTCA 420

72

73 TTACCTCACT ATGATTCAAC CGAGTGGGAA TGGATTAGAG GAGCTTTGGT TACGGTAGAC 480

74

75 AGAGACTATG GAATCTTGAA CAAGGTGTTT CACAACATAA CAGACACCCA CGTAGCACAC 540

76

77 CAC 543

78

79 (2) INFORMATION FOR SEQ ID NO:2:

80

81 (i) SEQUENCE CHARACTERISTICS:

82 (A) LENGTH: 544 nucleotides

83 (B) TYPE: nucleotide

84 (C) STRANDEDNESS: single

85 (D) TOPOLOGY: linear

86 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

87

88 TATAGGCACC GGAGGCACCA TTCCAACACA GGATCCCTCG AAAGAGATGA AGTATTTGTC 60

89

90 CCAAAGCAGA AATCCGCAAT CAAGTGGTAC GGCGAATACC TCAACAACCC TCCTGGTCGC 120

91

92 ATCATGATGT TAACTGTCCA GTTCGTCCTC GGATGGCCCT TGTACTTAGC CTTCAACGTT 180

93

94 TCTGGCAGAC CCTACAATGG TTTCGCTTCC CATTTCTTCC CCAATGCTCC TATCTACAAC 240

95

96 GACCGTGAAC GCCTCCAGAT TTACATCTCT GATGCTGGTA TTCTAGCCGT CTGTTATGGT 300

97

98 CTTTACCGTT ACGCTGTTGC ACAAGGACTA GCCTCAATGA TCTGTCTAAA CGGAGTTCCG 360

99

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100	CTTCTGATAG TTAACCTTTTT CCTCGTCTTG ATCACTTACT TACAACACAC TCACCCTGCG	420
101		
102	TTGCCTCACT ATGATTCATC AGAGTGGGAT TGGCTTAGAG GAGCTTTAGC TACTGTAGAC	480
103		
104	AGAGACTATG GAATCTTGAA CAAGGTGTTC CATAACATCA CAGACACCCA CGTCGCACAC	540
105		
106	CACT	544

### (2) INFORMATION FOR SEQ ID NO:3:

#### (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	1855 nucleotides
(B) TYPE:	nucleotide
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

117		
118	ATGAAGCTTT ATAAGAAGTT AGTTTTCTCT GGTGACAGAG AAATTNTGTC AATTGGTAGT	60
119		
120	GACAGTTGAA GCAACAGGAA CAACAAGGAT GGTGGTGNT GATGCTGATG TGGTGATGTG	120
121		
122	TTATTCATCA AATACTAAAT ACTACATTAC TTGTTGCTGC CTACTTCTCC TATTTCCCTCC	180
123		
124	GCCACCCATT TTGGACCCAC GANCCCTCCA TTAAACCCT CTCTCGTGCT ATTCACCAGA	240
125		
126	AGAGAAGCCA AGAGAGAGAG AGAGAGAATG TTCTGAGGAT CATTGTCTTC TTCATCGTTA	300
127		
128	TTAACGTAAG TTTTTTTTGA CCACTCATAT CTAAAATCTA GTACATGCAA TAGATTAATG	360
129		
130	ACTGTTCCCT CTTTTGATAT TTTCAGCTTC TTGAATTCAA GATGGGTGCT GGTGGAAGAA	420
131		
132	TAATGGTTAC CCCCTCTTCC AAGAAATCAG AAAGTGAAGC CCTAAAACGT GGACCATGTG	480
133		
134	AGAAACCACC ATTCAGTGT AAAGATCTGA AGAAAGCAAT CCCACAGCAT TGTTTCAAGC	540
135		
136	GCTCTATCCC TCGTTCTTTC TCCTACCTTC TCACAGATAT CACTTTAGTT TCTTGCTTCT	600
137		
138	ACTACGTTGC CACAAATTAC TTCTCTCTTC TTCCTCAGCC TCTCTCTACT TACCTAGCTT	660
139		
140	GGCCTCTCTA TTGGGTATGT CAAGGCTGTG TCTTAACCGG TATCTGGGTC ATTGGCCATG	720
141		
142	AATGTGGTCA CCATGCATTC AGTGACTATC AATGGGTAGA TGACACTGTT GGTTTTATCT	780
143		
144	TCCATTCCTT CCTTCTCGTC CCTTACTTCT CCTGGAAATA CAGTCATCGT CGTCACCATT	840
145		
146	CCAACAATGG ATCTCTCGAG AAAGATGAAG TCTTTGTCCC ACCGAAGAAA GCTGCAGTCA	900
147		
148	AATGGTATGT TAAATACCTC AACAAACCTC TTGGACGCAT TCTGGTGTTA ACAGTTCAGT	960
149		
150	TTATCCTCGG GTGGCCTTG TATCTAGCCT TTAATGTATC AGGTAGACCT TATGATGGTT	1020
151		
152	TCGCTTCACA TTTCTTCCCT CATGCACCTA TCTTTAAAGA CCGAGAACGC CTCCAGATAT	1080

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153
154 ACATCTCAGA TGCTGGTATT CTAGCTGTCT GTTATGGTCT TTACCGTTAC GCTGCTTCAC      1140
155
156 AAGGATTGAC TGCTATGATC TGCCTCTATG GAGTACCGCT TTTGATAGTG AACTTTTTTCC      1200
157
158 TTGTCTTGGT AACTTTCTTG CAGCACACTC ATCCTTCGTT ACCTCATTAT GATTCAACCG      1260
159
160 AGTGGAATG GATTAGAGGA GCTTTGGTTA CGGTAGACAG AGACTATGGA ATATTGAACA      1320
161
162 AGGTGTTCCA TAACATAACA GACACACATG TGGCTCATCA TCTCTTTGCA ACTATACCGC      1380
163
164 ATTATAACGC AATGGAAGCT ACAGAGGCGA TAAAGCCAAT ACTTGGTGAT TACTACCACT      1440
165
166 TCGATGGAAC ACCGTGGTAT GTGGCCATGT ATAGGGAAGC AAAGGAGTGT CTCTATGTAG      1500
167
168 AACCGGATAC GGAACGTGGG AAGAAAGGTG TCTACTATTA CAACAATAAG TTATGAGGCT      1560
169
170 GATAGGGCGA GAGAAGTGCA ATTATCAATC TTCATTTCCA TGTTTTAGGT GTCTTGTTTA      1620
171
172 AGAAGCTATG CTTTGTTTCA ATAATCTCAG AGTCCATNTA GTTGTGTTCT GGTGCATTTT      1680
173
174 GCCTAGTTAT GTGGTGTCGG AAGTTAGTGT TCAAACGCT TCCTGCTGTG CTGCCAGTG      1740
175
176 AAGAACAAGT TTACGTGTTT AAAATACTCG GAACGAATTG ACCACAAANAT ATCCAAAACC      1800
177
178 GGCTATCCGA ATTCCATATC CGAAAACCGG ATATCCAAAT TTCCAGAGTA CTTAG      1855
179

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

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183 (A) LENGTH: 384 amino acids
184 (B) TYPE: amino acid
185 (C) STRANDEDNESS:
186 (D) TOPOLOGY: linear
187

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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190
191 Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser
192 1 5 10 15
193
194 Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr
195 20 25 30
196
197 Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Lys Arg Ser
198 35 40 45
199
200 Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser
201 50 55 60
202
203 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
204 65 70 75 80
205

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206	Leu	Ser	Thr	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Val	Cys	Gln	Gly	Cys
207					85					90					95	
208																
209	Val	Leu	Thr	Gly	Ile	Trp	Val	Ile	Gly	His	Glu	Cys	Gly	His	His	Ala
210				100					105					110		
211																
212	Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	Val	Gly	Phe	Ile	Phe	His
213			115					120					125			
214																
215	Ser	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg
216		130					135					140				
217																
218	His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	Asp	Glu	Val	Phe	Val	Pro
219	145					150					155					160
220																
221	Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	Lys	Tyr	Leu	Asn	Asn	Pro
222				165						170					175	
223																
224	Leu	Gly	Arg	Ile	Leu	Val	Leu	Thr	Val	Gln	Phe	Ile	Leu	Gly	Trp	Pro
225				180						185				190		
226																
227	Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala
228			195					200					205			
229																
230	Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	Lys	Asp	Arg	Glu	Arg	Leu
231		210					215					220				
232																
233	Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
234	225					230					235					240
235																
236	Tyr	Arg	Tyr	Ala	Ala	Ser	Gln	Gly	Leu	Thr	Ala	Met	Ile	Cys	Val	Tyr
237				245						250				255		
238																
239	Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	Leu	Val	Leu	Val	Thr	Phe
240				260					265					270		
241																
242	Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp
243			275					280					285			
244																
245	Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
246		290					295					300				
247																
248	Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
249	305					310					315					320
250																
251	Leu	Phe	Ala	Thr	Ile	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Glu	Ala
252					325					330					335	
253																
254	Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	Phe	Asp	Gly	Thr	Pro	Trp
255				340					345					350		
256																
257	Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Leu	Tyr	Val	Glu	Pro
258			355					360					365			

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/885,189**

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Line	Error	Original Text
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**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/09/885,189**

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*INPUT SET: S36845.raw*

< < THERE ARE NO ITEMS MISSING > >

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**SEQUENCE CORRECTION REPORT**  
**PATENT APPLICATION US/09/885,189**

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Line	Original Text	Corrected Text
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